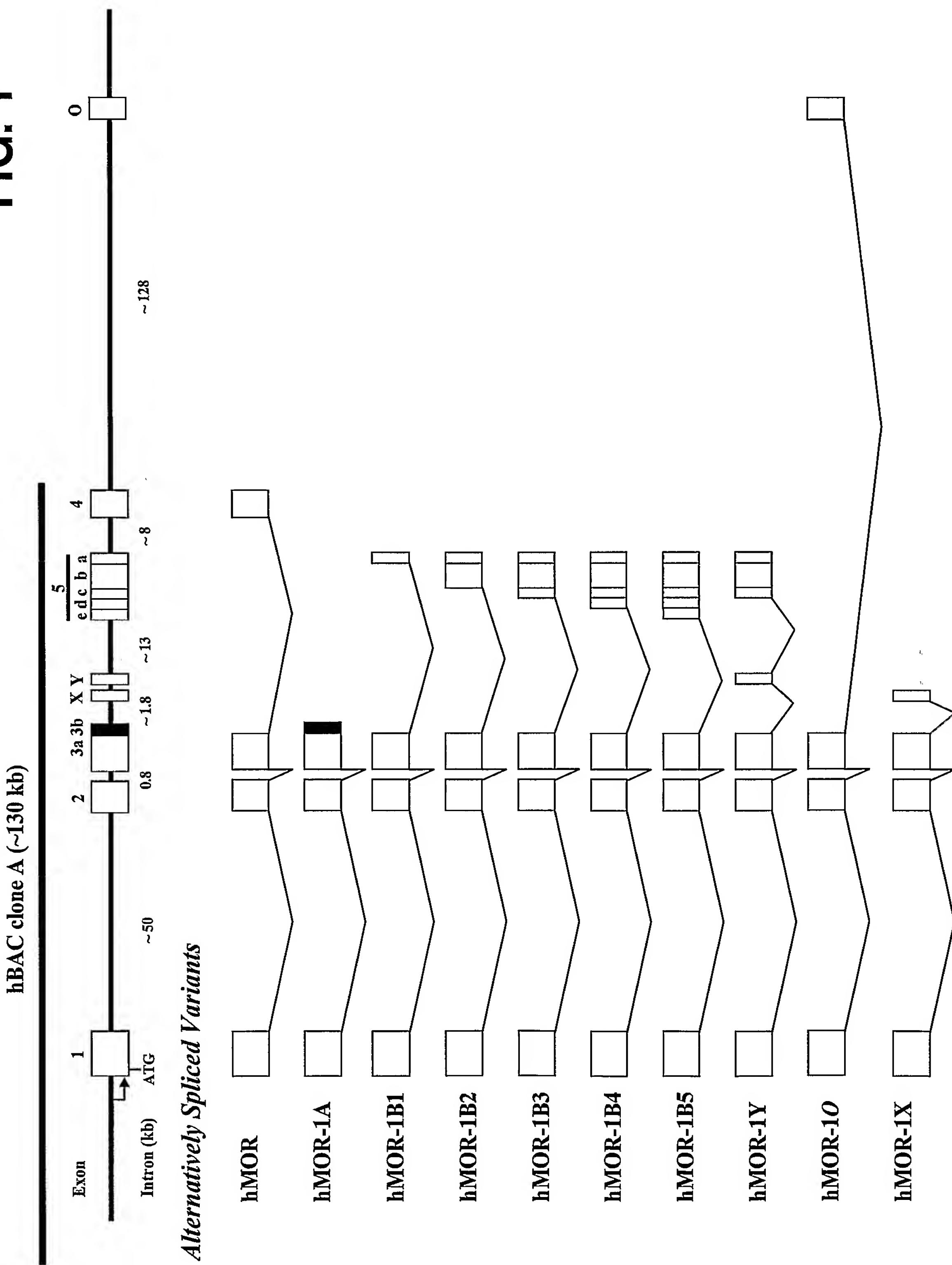


*Genomic Structure of the human mu opioid receptor gene***FIG. 1**

hMOR-1A

Exon 3a ↓ **Exon 3b**

---ACTAATCATCAGGTACGGCAGTCTAGAATTAGGTATCTACTGGGATGACATAAAAATTATAAGGGCTT
 T N H Q V R S L * (SEQ ID NO: 27)
 TGTGCTAAACTAGGAGTTAATCCATTATAGAGGAATGGAGGAAGGGAAAGCAAGGG (SEQ ID NO: 28)

hMOR-1B1

Exon 3a ↓ **Exon 5a**

---ACTAATCATCAGAAAATAGATTCAAAAGTCATCTTACTCAACTGTGAGCATAACCAAGGGCTAATA
 T N H Q K I D L F Q K S **S[#]** L L N C E H T K G * (SEQ ID NO: 29)
 ATTACAATTTCCCGTGAAGAATAAGATTGGAAGC (SEQ ID NO: 30)

hMOR-1B2

Exon 3a ↓ **Exon 5b**

---ACTAATCATCAGAGAGAAAGAGACAGAAATCTTGACTGGIAAGAAATTGTTIACCCCTTTGCCAGGCCA
 T N H Q R E R R Q K **S[#]** D W * (SEQ ID NO: 31)
 GGCTTCTGGTTCCCTTCCCTGAGCGGCCCTAGTGAATCCCTAACACACACAGAAAACGACCTCATAACACAAAA--- (SEQ ID NO: 32)

hMOR-1B3

Exon 3a ↓ **Exon 5c**

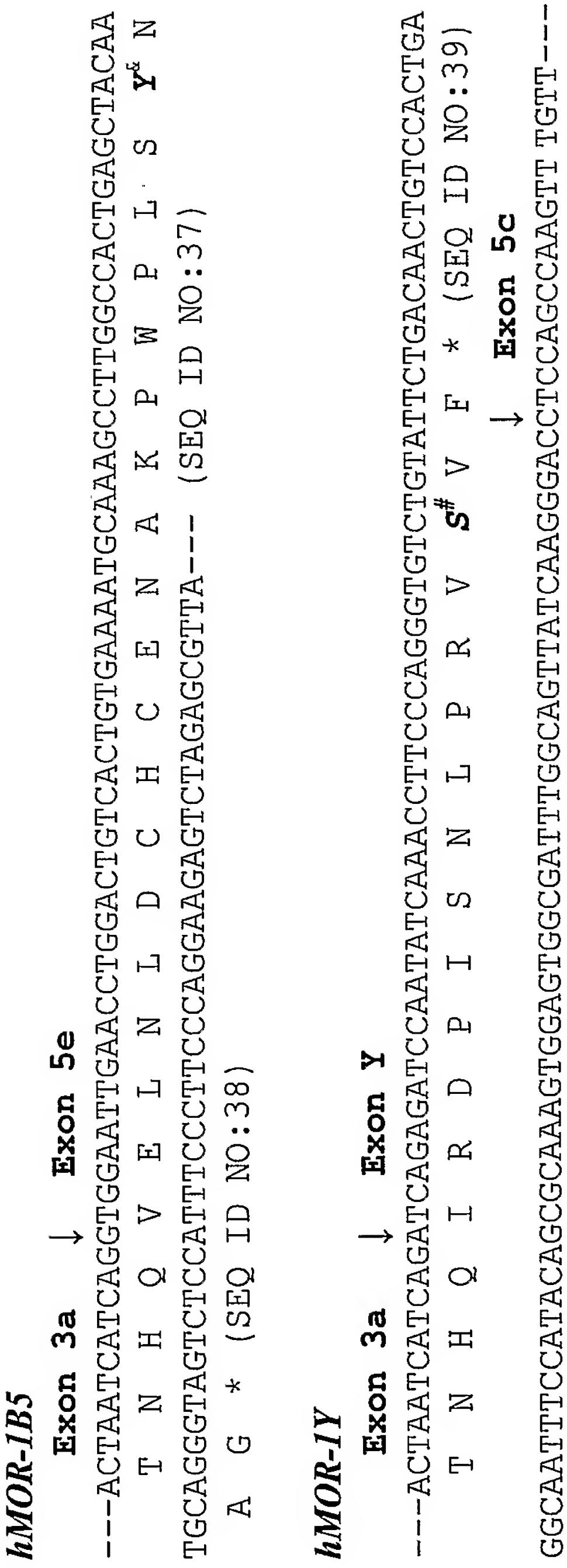
---ACTAATCATCAGGGACCTCCAGCCAAAGTTGCTTGACCAAATGCCGCGGTCTGAAAGGGGGCTT
 T N H Q G P A K F V A D Q L A G S S * (SEQ ID NO: 33)
 ACAGGTGTTCCAAGCCCGTGTGTTTATCCTGAAGTATCCCTAACACACACAGAAAACGACCTCATAACACAAAA--- (SEQ ID NO: 34)

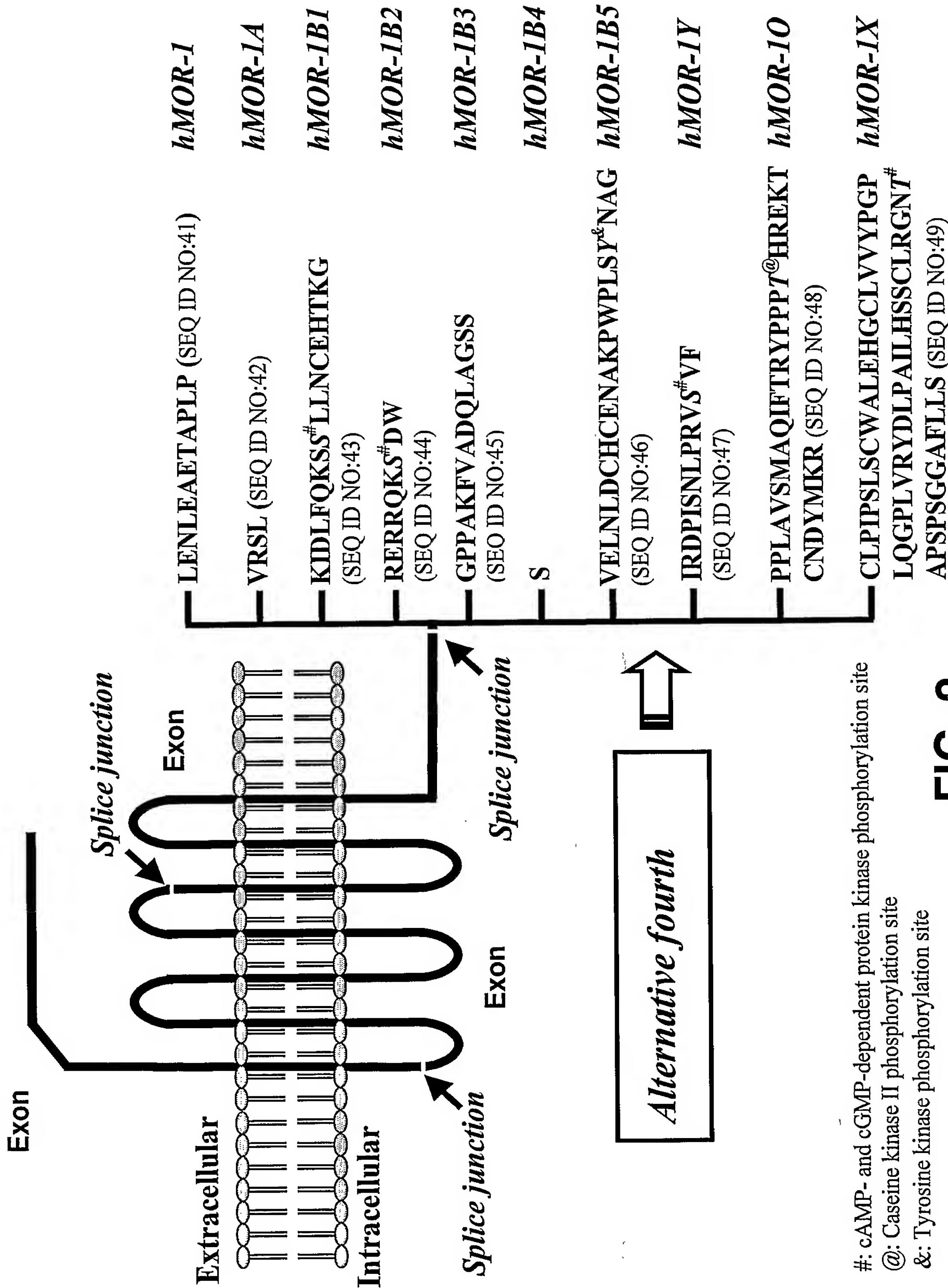
hMOR-1B4

Exon 3a ↓ **Exon 5d**

---ACTAATCATCAGAGCTGACTATGACATGAACCCCTAAATTCCCTGTTCCC--- (SEQ ID NO: 35)
 T N H Q S * (SEQ ID NO: 36)

FIG. 1B(1)

**FIG. 1B(2)**



2
EIG

hMOR-1B1 (1354 bp)

hMOR-1B1 (406 aa)

MDSSAAPTNASNCTDALAYSSCSPAPSPCGSWVNLSHLDGNLSDPCCGPNRTDLCGRDSLCPPTGSPSSMITAITIMALYSIVCWW
GLFGNFLVMMYVIVRYTKMKTATNIYIFNIALADALATSTLPFQSVNNYLMGTWPFGTILCKIVISIDYVYNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKINVCNWIISSAIGLPVMMATTKQYRQGSIDCILTFSHPTTWYWWENLLKICVFIFAFIMPVLIITV
CYGLMILRKSSVRMLSGSKEKDRNLRIRTRMVLVVAVFIVCWTPIHIYVIKALVVTIPETTFQTVSSWHFCIALGYTNSCLNPV
TYAFIDNEFKRCEREECPTSSNIEOONNSTRIRONTRDHIPSTANTVDRINHOKIDIFOKSSLLNCEHTIKG (SEQ ID NO:51)

FIG. 3A

hMOR-1B2 (2218 bp)

FIG. 3B(1)

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hMOR-1B2 (397 aa)

MDSSAAPTNASNCTDALAYSSCSPGSPWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITIMALYSIVCVV
GLFGGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKINVCNWLSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENILKICVFIFAFIMPFVLLITY
CYGLMILRLKSVRMLSGSKEKDRNLRIRTRMVLVVVAVFIVCWTPHIYVIIKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIPPTSSNIEQQNSTRRQNTRDHPSTANTVDRTNHQERRRQKSDW
(SEQ ID NO:53)

FIG. 3B(2)

hMOR-1B3 (2483 bp)

FIG. 3C(1)

GTCCAAAATCCAACTATAAGAACATAAGAATGTGAGAGGCAGCACATAAGTCAAGAAATAAGCATTATTTCAT
GGACCAATATGATAAAAGCCATCTAACCC (SEQ ID NO:54)

hMOR-1B3 (403 aa)

MDSSAAPTNAASNCTDALAYSSCSPGSPWVNLSHLDGNLSDPCGPNRRTDLGGRDSLCPPTGSPSMITA
GLFGNFLVMYVIVRYTKMKTKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVVISIDYNNMFTSIFT
YIAVCHPVVKALDFRTPRNAAKINVCNWISSAIGLPVMMATTKYRQGSIDCTLTFSHPTWYWENLLKICV
CYGLMLRLKSVRMLSGSKEKDRNLRITRMVLVVVAVFIVCWTPHIYVIIKALVTPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREEFCPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQGPPAKFVADQLAGSS (SEQ ID NO:55)

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FIG. 3C(2)

hMOR-1B4 (1251 bp)

hMOR-1B4 (389 aa)

MDSSAAPTNASNCTDALLYSSCCSPAPSPGSWVNLSHLDGNLSDPCKPNRTDLGGGRDSLCPPTGSPSMSMITAITIMALYSIVCVV
GLFGNFLVMYVIRRRTKMKTTATNIYVFNLA DALATSTLPPFQSVNYILMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVD
RYIAVCHPVKALDFRTPRNAKIIINVCNWILSSAIGLPVMMATTKYRQGSIDCTLTFSHPTWYWE NLLKJCVFIFMPVLIIT
VCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTPIHYVIKALVTIPETTFQTVSWHFCIALGYTNSCLNLP
VLYAFLDENFKRCFREFCIPPTSSNIEQQNSTRJQRQNTRDHPSTANTVDRTNHQSQ (SEQ ID NO:57)

3D FIG

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hMOR-1B5 (1402 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCGGTCAGTACCTGGACAGCAGCCCCACGGAAACG
 CAGCAATTGGCACTGATGGCTTGGGTTACTCAAGTTGCTCCCCAGCAACCCAGCCCCAGCAACTGGTCCCCA
 CTTAGATGGCAACCTGTCGCCACCCATGGGGTCCGAACCGACCTGGGGAGAGACAGCCTGGCTCCGAC
 CGGCAGTCCCTCCATGATCACGGCATCACGATCATGGCCCTACTCCATCGTGTGCCATTCAGAAGACTGGC
 TCTGGTCATGTTGATTGTCAAGATAACACATCACATTACCTAACACATGGGAACATGGCCATTGGAAACCATCCTT
 AGATGGCTTAGCCACCGTACCCCTGGCTACCCATTAGATTACATGGCTACCCAGCATATTCAATGGCTGATCGAT
 TGCAAGGATAGTGAATTACTATAACATGGTCAAGGGCTTAGATTCCATGGCTACCCCTGGCTACCTGGCAAGGAAATGGC
 ACATTGGCAGTCTGCCACCCCTGTCAAGGCCATTGGCTTCCCTGTAATGTTCATGGCTACCAAAATAACAGGCAAGG
 GATGCCCTCTCAGCCATGGCTTCCCTGTAATGTTCATGGCTACCTGGTACTGGAAAGATCTGTGTTCATCTGGCTTCC
 TAACATTCTCATCCAAACCTGGTGGCTATGGACTGATGATGTTGACTGGGAAACCTGCTGCTGGGACT
 CTCATCATTACCGTGTGGCTATGGACTGATGATGATGTTGACTGGGAAACCTGCTGCTGGGACT
 ACAGGAATCTCGAAGGATCACCGGATGGCTGGGTGGCTGGGTGGCTGGGACT
 TTACGGTCATCATTAAAGGCTTGGTTACAATCCCAGAAACTACGGTCCAGAAGACTGGCATTGGCTCATGGCT
 GTTACACAAACAGCTGCCCTAACCCAGTCCTAACAAACACTCCACTCGAATTGGTCAAGAACACTAGAGACC
 TATCCCAACCTCTCCAAACATGGCAATTGAGAACATAATCATCAGGTGGAAATTGAAACCTGGACTGTCA
 AATACAGTGGATAGAACATAATCATCAGGTGGAAATTGAAACCTGGACTGTCAACTGGCTTAATT
 AGCTACAAATGGCAGGGTAGTCTCCATTCCAGGAAGAGTCTAGAGGCTGACTATGACATGAACCCCTAA
 ACTATTTCATATGATTAGAGCTGACTATGACATGAACCCCTAAATTCCCTGTTCCC (SEQ ID NO:58)

hMOR-1B5 (410 aa)

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MDSSAAPTINASNCTTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDILGGRDSLCPPTGSPSMITA
 ITMALYSIVCVVGLFGGNFLVMMYVIVRYTKMKTAATNIYIFNLALADALATSTL
 PFQSVNYLMGTWPFGTILCKIVVISIDYYNMFTSIFTLCTMSVDR
 YIAVCHPVKAALDFRTPRNAAKINVCNWLSSAIGLPVMFMATT
 KYRQGSIDCILTFSHPTWYWENLLKICVFIFAFIMPVLIIV
 CYGLMLRLKSVRMLSGSKEKDRNLRJTRMVLVVVAVFIVCWT
 PIHYVIKALVTIPETTFQTVSWHFCLGTYTNCLNPV
 LYAFLDENFKRCFREFCIPSSNIEQQNSTRIRQNTRDHP
 STANTVDRNHLQVIELNLDCHCENAKPWPLSYNAG (SEQ ID
 NO:59)

FIG. 3E

hMOR-1Y (2601 bp)

FIG. 3F(1)

AGTTGCAATCCATGGAGGAATGCTGATAACCTCGGTGATAAGATAAAAAACCAAGCATACTAGAAGTGTCTCTAA
ATTAAAAATACAGTAGTTGCTAGAGAAAATTAGTCCAAAACATAGAAATGTGAGAGGGTAGC
ACATAAGAAATAAGTCATGGGGATTATTTCATGGACCAATATGATAAAAGCCATCTAACCAAGGGC
(SEQ ID NO:60)

hMOR-1Y (402 aa)

MDSSAAPTNASNC'TDALAYSSCSPGSPAPSPGSPWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITATIMALYSIVCVV
GLFGGNFLVMMYVTVRYTKMKTKTATNITYIFNLFNLALADALATSTLIPFQSVNNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKINVCNWLSSAIGLPPVMMFMAKKYRQGSIDCTLTFSHPTWYWENLLKICCVFIFAFIMPVLITV
CYGLMILRLKSVRMLSGSKEKDRLNLRIRTRMVLVVAVFIVCWTPIHYVIKALVTIPETTFQTVSWHFCIALGYTNNSCLNPV
LYAFLDENFKRCFREFCIPTSSNIEQQQNSTRIRQNTRDHPSTANTVDRTNHQIRDPISNLPRVSVF (SEQ ID NO:61)

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FIG. 3F(2)

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hMOR-1	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1A	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1B1	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1B2	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1B3	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1B4	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1B5	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1O	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1X	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
hMOR-1Y	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP
Consensus	(1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWWVNLSHLDGNLSDPCCGNRTDLGGRDSLCP

120

61

hMOR-1	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1A	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B1	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B2	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B3	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B4	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1B5	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1O	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1X	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
hMOR-1Y	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT
Consensus	(61) PTGSPSMSMITAITIMALYSIVCVVGLFGNFLVMMYIVRYTCKMKTATNIYIFNLALADALAT

FIG. 4(1)

121

180

hMOR-1 (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-1A (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-1B1 (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-1B2 (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-1B3 (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-1B4 (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-1B5 (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-10 (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-1X (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 hMOR-1Y (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF
 Consensus (121) STLPFQSVNVLMGTPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCCHPVKALDF

181

240

hMOR-1 (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-1A (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-1B1 (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-1B2 (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-1B3 (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-1B4 (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-1B5 (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-10 (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-1X (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 hMOR-1Y (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
 Consensus (181) RTPRNAKIIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI

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FIG. 4 (2)

241

300

301

360

hMOR-1	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1A	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B1	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B2	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B3	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B4	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1B5	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1O	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1X	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
hMOR-1Y	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI
Consensus	(301) YVIIKALVTTIPETTFQTVSWHFCIALGYTN SCLNPVLYAFLDENFKRCFREFCIPTSSNI

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FIG. 4(3)

361

420

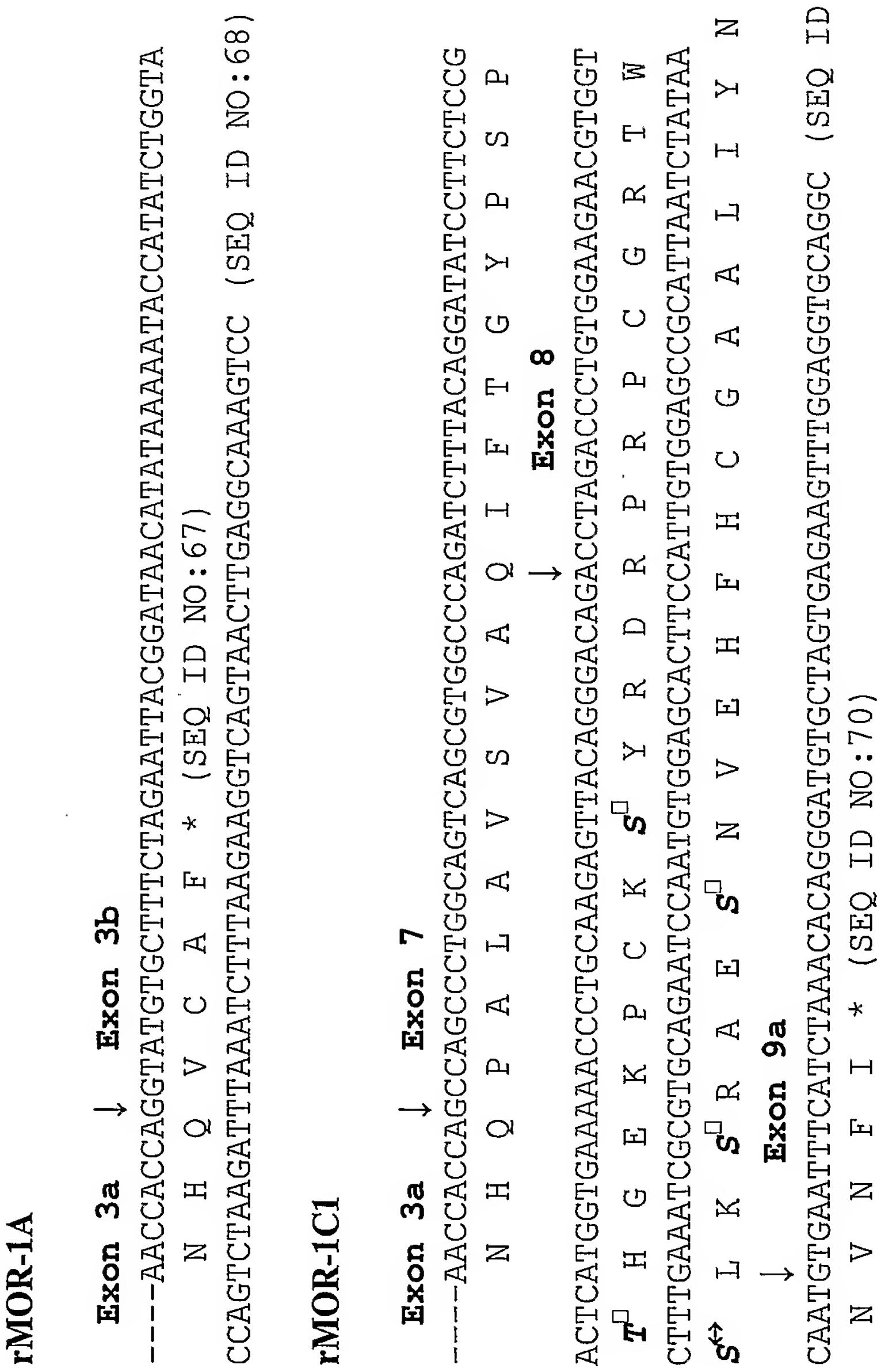
hMOR-1 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQLENLEAETAPLPLP-----
 hMOR-1A (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQVRSLS-----
 hMOR-1B1 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQKIDLFQKSSLLNCEHTKG-----
 hMOR-1B2 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQERRQKSDW-----
 hMOR-1B3 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQGPPAKFVADQLAGSS-----
 hMOR-1B4 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQQS-----
 hMOR-1B5 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQVELNLDCHCENAKPWPLSYNAG-----
 hMOR-1O (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQPPPLAVSMAQIFTRYPPPTHREKTCNDYMKR-----
 hMOR-1X (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQCLPISLSCWALEHGCLVWYPGPLQGPLVRYD-----
 hMOR-1Y (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQIRDPISNLPRVSVF-----
 Consensus (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQ

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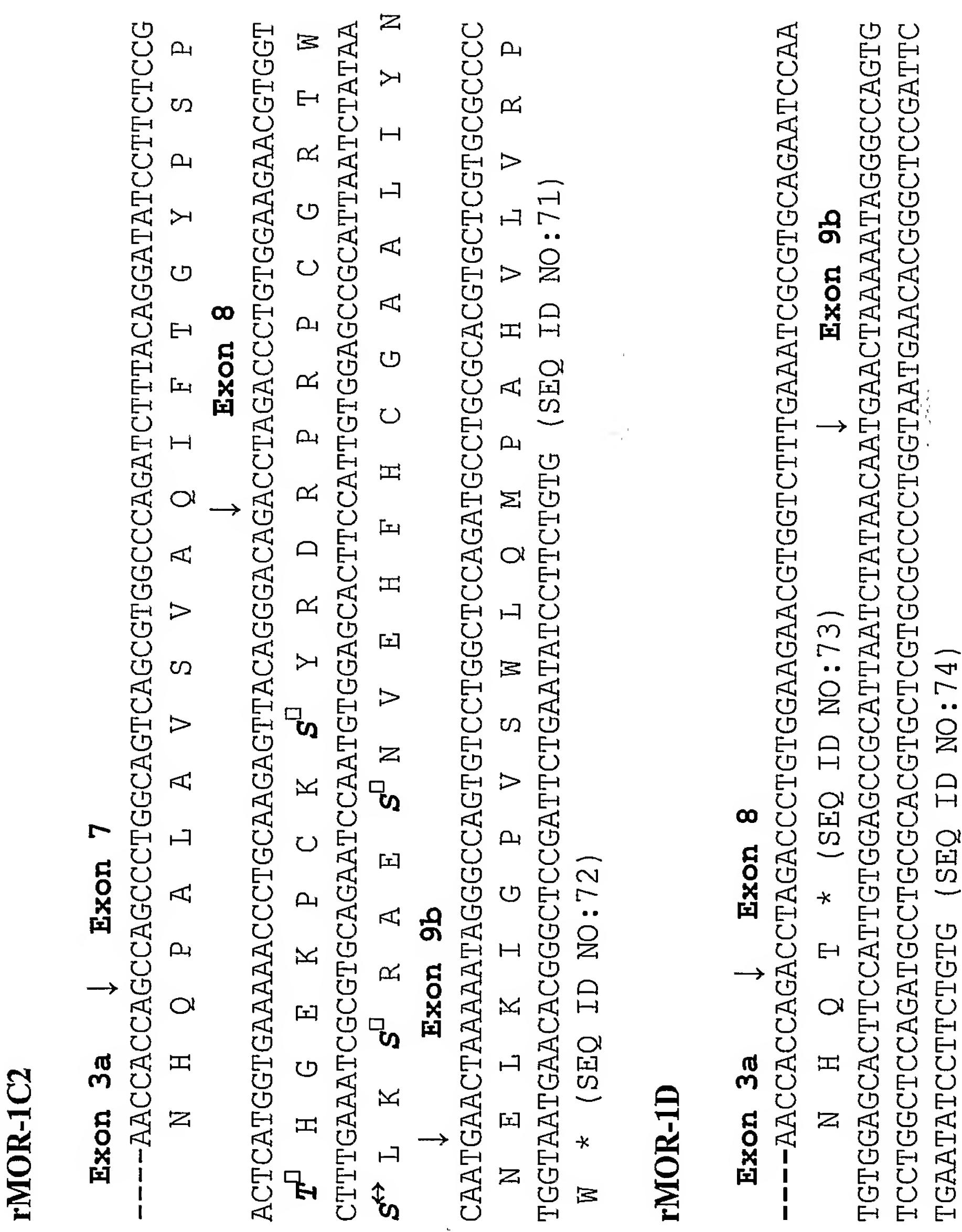
421 446
 hMOR-1 (401) ----- (SEQ ID NO:62)
 hMOR-1A (393) ----- (SEQ ID NO:63)
 hMOR-1B1 (407) ----- (SEQ ID NO:51)
 hMOR-1B2 (398) ----- (SEQ ID NO:53)
 hMOR-1B3 (404) ----- (SEQ ID NO:55)
 hMOR-1B4 (390) ----- (SEQ ID NO:57)
 hMOR-1B5 (411) ----- (SEQ ID NO:59)
 hMOR-1O (419) ----- (SEQ ID NO:64)
 hMOR-1X (421) LPAILHSSCLRGNTAPSPPSGGAFLLS (SEQ ID NO:65)
 hMOR-1Y (403) ----- (SEQ ID NO:61)
 Consensus (388) ----- (SEQ ID NO:66)

FIG. 4(4)

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**FIG. 5(1)**

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**FIG. 5(2)**

rMOR-1B2

Exon 3a → Exon 5b

rMOR-1E

→ **Exon 3a** **Exon E**

-----AACCACGGAGCAGATTAGGATTATAACAAAAGACTACCACG'TCAGAGG
N H Q G A E L * (SEQ ID NO: 77)
AGCAGCCAGGGAGGCCCTGGCCCCAACATGGTAGGTGCTCCCACACTCTCAC
TTTCAGCTATGGCTACCCGGCATAGCCTTATTCAAGTCAGTCTGACTGAC
GGAGACAGGAATGCTCATACCGAAGTGGTAATGCAATACACGTTGAGCG
GCAGAGTCAATCCCCACTCAAAGGCAATTAAACAAATTAAACAAAT
CTCTGTGCCATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CTTTCTAAGCAGCCCTTTAGGGTTCAAACCTCGCCTGCACATTGAGGAT
TTTCCAACCCAGGATAACATCTAGAGCAAGCAATTGAAACTATACAA
TGCTTCATTGGAGAAAGGAGCATAGGAAGGAAAGGCTTGGCTCTCC
TGTAGGGGTGCTGGCTGCTAGCTTCCCTAGGTGCTTGTCCAGGCT
AACCTCTATTCCAGCACATTCCAGC (SEQ ID NO: 78)

FIG. 5(3)

rMOR-1B2 (1628 bp)

rMOR-1B2 (394 aa)

FIG. 6A

rMOR-1C1 (1433 bp)

rMOR-1C1 (451 aa)

MDSSTGPGNTSDCSDPLAQASCSPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDLCPQQTGSPSMVTAITIMALYSIVCVVG
LFGNFLVMMYVTVRYTKMKTATNIYIFNLALADALATSTLPFQSVNNYLMGTTWPFGTLCKIVISIDYNNMFTSIFTLCTMSVDRY
IAVCHPVKADEFRTPRNAKIVNVCNWILSSAIGLPPVFMATTKYRQGSIDCCTLTFSHPTWYWENLLKICVFIFAFIMPFVLIITV
CYGLMLRLKSVRMLSGSKEKDRNLRITRMVLVVVAVFIVCWTPIHYYVNIKALITIPETTFQTVSWHFCLALGYTNSCLNPVLT
YAFLDENFKRCFREFCIPPTSSTIEQQNSTRVRQNTREHPSTANTVDRTNHQPALAVSVAQIFTGYPSPTHGEKPCKSYRDRPRP
CGRTWSLKSRAESNVEHFHCGAALIYNNVNEI (SEQ ID NO:82)

FIG. 6B

rMOR-1C2 (1480 bp)

rMOR-1C2 (468 aa)

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MDSSPGGNTSDCSDPLAQASCSPAPGSWLNLSHVDCGNQSDPCGGLNRTGLGGNDSSLCPQTGSPSMVTAITIMALYSIVCVVG
LFGNFLVMMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNNYLMGTTWPFGTILCKIVVISIDYYNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPPVMMATTKYRQGSIDCTLTFSHPTTWYWWENLLKICVFIFAFIMPRP
CYGLMILRLKSSVRMLSGSKEKDRNLRJTRMVLVVAVFIVCWTPIHIYVIIKALITIPETTFQTVSWHFCIALGYTNSCLNPVVL
YAFLDENFKRCREFCIPTSSSTIEQQNSTRVRQNTREHPSTANTVDRINHQPALAVSVAQIFITGYPSPTHGEKPCKSYRDRPRP
CGRTWSSLKSRAESNVEHHFCGAALIYNNELKIGPVSWLQMPAHVLRPW (SEQ ID NO:84)

FIG. 6C

rMOR-1D (1385 bp)

rMOR-1D (387 aa)

MDSSSTGPGNTSDCSDPLAQASCSPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDLCPQTTGSSPSMVTAIMALYSIVCVVG
LFGNFLVMMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRY
IAVCHPVKAIDFRTPRNAKIVNVCNWILSSAIGLPPVMEFMAITKQGSIDCCTLTFSHPTWYWENLLIKICVFVFAFIMPVLIITV
CYGLMLRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTPIHIYVMIKALITIPETFQTVSWHFCIALGYTNSCLNPVLYAFLD
DENFKRCREFCIPTSSSTIEONSTRVRONTREHPSTANTVDRTNHOT (SEQ ID NO:86)

Fig. 6D

rMOR-1E (2078 bp)

GTTACAGCCTACCTAGTCCGCAGGCACCATGGACAGCAGGCCCTCAGGCC
 CAGACCCCTTAGCTCAGGCAAGTTGCTCCAGCACCTGGCTCACA
 CGATCCATGCGGTCTGAACCGCAGGGCTTGGGGAAACGACAGCCTGC
 CACAGCCATTACCATCATGGCCCTACTCTATCGTGTAGTGGC
 TTGTAAGATAACCAAAATGAAGAGACTGCCAACATCTACATTTCA
 TACACTGCCCTTCAGAGTGTCAACTACCTGATGGGAACATGGCC
 TACAGGCAACATGGGATTTCCGTACCCGATATTCA
 ATAGATTACTACACATGGTCACTGGATTTCCGTACCCGAA
 CAGTCAAAGCCCTGGTAAATGGCAACCACAAATCTGGTCTT
 CGGTCTGGCTGTAATGGTCATGGCAACCTGCTCAA
 ACCTGGTACTGGAGAACCTGCTGTTATCTCGCTT
 TTACGGCCTGATGATGATCTACGACTCAAGAGCG
 GATCACCCCCGGATGGTGGTGGCTGTGTATTATCGT
 GCGCTGATCACGATTCCAGAACACATTCA
 GCCTGAATCCAGTTACGCCCTCAGAGTCCACTCGAG
 ACGATCGAACAGCAAAACTCCACTCGAGTCCGT
 ACTAACCCAGGGAGCAGAGTTATGAGGATTAA
 GGGCCCTGGCCCCACAAATGGTAGGGTGGCT
 GCTATGGCTACCCGGCATAGCCTTATTCA
 CTCAAGGAGACAGGAATGCTCAT
 CATGGTGGTAATGGGGCAGAGTCAT
 ACTAACCCAGGGAGCAGAGTTATGAGGATTAA
 GGGCCCTGGCCCCACAAATGGTAGGGTGGCT
 GCTATGGCTACCCGGCATAGCCTTATTCA
 CTCAAGGAGACAGGAATGCTCAT
 CATGGTGGTAATGGGGCAGAGTCAT
 AATCAGAGCCAGACAGAAATGGGT
 CATTGTTATCCACATCAACACATAACCC
 ACTTTGAAAGGGTAAGGATTAAATGGAT
 TGAAACTATACAAACTGAGCT
 GGAAAGCTTGGCTCTCCCTAGGTG
 GTAGCTTCCTAGGGACACTG
 CCAGCACATCCCTGTT
 (SEQ ID NO:87)

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FIG. 6E(1)

rMOR-1E (390 aa)

MDSSSTGPGNTSDCSDPLAQASCSPAPGSWLNLSHVVDGNQSDPCCGLNRTGLGGNDSSLCPQTGSPSMVTAITIMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATMNYIFNLA DALA LATSTLPPFQSVNNYLMGTWPFGTILCKIVISIDYYNNMFITSIFTLCTMSVDRY
IAVCHPVKAJDFRTIPRNAAKIVVNVCNWILSSAIGLPVMMFMAATTKYRQGSIDCTLFSHPTWYWENILKICVFIFAFIMPVLITV
CYGLMILRLKSVRMLSGSKEKDRLNRGITRMVLVVVAFTIVCWTPIHYYVIIKKALITIPETTFQTVSSWHFCIALGYTNNSCLNPVL
YAFLDENFKRCFREFCIPTSSTHEQQQNSTRVRQNTREHPSTANTVDRNHQGAEL (SEQ ID NO:88)

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FIG. 6E(2)